SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: KAYAGAKI, Nobuhiko

YAGITA, Kideo OKUMURA, Ko

NAKATA, Motomi

(ii) TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF

(iii) NUMBER OF SEQUENCES: 31

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: McDermott, Will & Emery
- (B) STREET: 99 Canal Center Plaza, Suite 300
- (C) CITY: Alexandria
- (D) STATE: Virginia
- (E) COUNTRY: USA
- (F) ZIP: 22314
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/913,555
 - (B) FILING DATE: 19-SEP-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Bucca Ph.D., Daniel
 - (B) REGISTRATION NUMBER: 42,368
 - (C) REFERENCE/DOCKET NUMBER: 50356-150
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-756-8600
 - (B) TELEFAX: 202-756-8699
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 - Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser 1 5 10 15
 - Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Trp
 20 25 30
 - Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile Gly 35 40 45

Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met 65 70 75 80	
Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala 85 90 95	
Arg Ser Tyr Tyr Tyr Asp Gly Ser Pro Trp Phe Thr Tyr Trp Gly Gln 100 105 110	
Gly Thr Thr Val Thr Val Ser Ser 115 120	
(2) INFORMATION FOR SEQ ID NO:2:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 360 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA to mRNA	
(wit) GEOMENGE DEGENERATION GEO. ID NO. 2	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: GTGCAGCTGC AGGAGTCTGG ACCTGAGCTG GTGAAGCCTG GGGCCTCAGT GAAGATTTCC	60
	20
	80
	40
	00
TACGATGGTA GCCCCTGGTT TACTTACTGG GGCCAAGGGA CCACGGTCAC CGTCTCCTCA	60
(2) INFORMATION FOR SEQ ID NO:3:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: peptide	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly 1 5 10 15	
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr 20 25 30	

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile 35

Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Asp Asn Gly Lys Phe Lys 50 60

	Tyr	Tyr 50	Thr	Ser	Arg	Leu	His 55	Ser	Gly	Val	Pro	Ser 60	Arg	Phe	Ser	Gly	
	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Tyr	Ser	Leu	Thr	Ile 75	Ser	Asn	Leu	Glu	Pro 80	
	Glu	Asp	Ile	Ala	Thr 85	Tyr	Phe	Cys	Gln	Gln 90	Tyr	Ser	Glu	Phe	Pro 95	Trp	
	Thr	Phe	Gly	Gly 100	Gly	Thr	Lys	Leu	Glu 105	Ile	Lys	Arg					
(2)	NFO	TAMS	ION 1	FOR S	SEQ 1	D NO	0:4:										
	(i)	(A) (B) (C)	LEI TYI STI	NGTH PE: r RANDI	ARACT : 324 nucle EDNES	bas eic a SS: c	se pa acid doubl	airs									
•	(ii)	MOLE	ECULI	E TYI	PE: 0	DNA	to r	nRNA									
	'xi)	SEOI	TENC	פשר ב	SCRIE	יים דיים	J. SI	70 TI	NO.	. 4 .							
GACAT											יייטייני	GGA	a cz	AG A Gr	רכאכנ	٦.	60
ATCAC																	120
GATGO	AACI	rg Ti	raaa(CTCCT	r GAT	CTAC	CTAC	ACAT	CAAC	AT T	racao	CTCAC	G AC	TCC	CATC	Ą	180
AGGTI	CAGI	rg go	CAGTO	GGT	C TGC	GAC	AGAT	TATT	CTC	rca (CCATO	CAGC	AA CO	CTGG	AACC'	ŗ	240
GAAGA	TATI	rg co	CACT	[ACT]	r TTC	TCAC	GCAA	TATA	AGTG	L TA	TCCC	GTGG#	AC GI	TCGC	STGG	Ą	300
GGCAC	CAAC	GC TO	GAA	ATCAZ	A ACC	3G											324
(2)]	NFOF	TAMS	ON I	FOR S	SEQ I	D NO	0:5:										
	(i)	(A) (B) (C)	LEN TYI STI	NGTH: PE: a RANDE	ARACT : 118 amino EDNES GY:]	3 ami 5 aci 5S: s	ino a id sing]	acids	5								
((ii)	MOLE	ECULI	E TYI	E: p	epti	ide										
						•											
((xi)	SEQU	JENCI	E DES	SCRIE	OIT	N: SE	EQ II	NO:	:5:							
	Val 1	Gln	Leu	Gln	Gln 5	Ser	Gly	Ala	Glu	Leu 10	Val	Arg	Pro	Gly	Thr 15	Ser	
	Val	Lys	Met	Ser 20	Cys	Lys	Ala	Ala	Gly 25	Tyr	Thr	Phe	Thr	Asn 30	Tyr	Trp	
	Ile	Gly	Trp 35	Val	Lys	Gln	Arg	Pro 40	Gly	His	Gly	Leu	Glu 45	Trp	Ile	Gly	
	Tyr	Leu 50	Tyr	Pro	Gly	Gly	Leu 55	Tyr	Thr	Asn	Tyr	Asn 60	Glu	Lys	Phe	Lys	
	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ser	Ser	Thr	Ala	Tyr	Met	

65					70					75					80	
Gln	Leu	Ser	Ser	Leu 85	Thr	Ser	Glu	Asp	Ser 90	Ala	Ile	Tyr	Tyr	Cys 95	Ala	
Arg	Tyr	Arg	Asp 100	Tyr	Asp	Tyr	Ala	Met 105	Asp	Tyr	Trp	Gly	Gln 110	Gly	Thr	
Thr	Val	Thr 115	Val	Ser	Ser											
(2) INFO	RMAT:	ION I	FOR S	SEQ I	D NO	0:6:										
(i)	(B)	LEN TYI STI	IGTH PE: 1 RANDI	ARACT : 354 nucle EDNES GY: 1	bas ic a SS: c	se pa acid doubl	airs									
(ii)	MOLI	ECULI	E TYI	PE: 0	DNA	to r	nRNA									
(xi)	SEQU	JENCI	E DES	SCRIE	OITS	1: SI	EQ II	ONO:	6:							
GTGCAGCT	GC A	GCAGT	CAG	AGC	CTGAC	CTG	GTA	AGGC	CTG (GGACI	TCAC	GT GA	AAGAT	rgtco	2	60
TGCAAGGC'	rg C	rgga:	CACA	C CTI	CACT	TAAC	TAC	rgga:	rag (STTGO	GTA	AA G	CAGAC	GCC:	ľ	120
GGACATGG	CC T	rgag:	rgga:	r TGC	ATA	CTT	TAC	CCTGC	GAG (GTCTT	TAT	AC T	AACTA	ACAA:	r	180
GAGAAGTT	CA AC	GGCZ	AAGG	CAC	CACTO	ACT	GCA	GACA	CAT (CCTCC	CAGC	AC AG	GCCT	ACATO	3	240
CAGCTCAG	CA GO	CCTG	ACATO	C TGA	AGGA	CTCT	GCC	ATCT	ATT A	ACTGT	rgca <i>i</i>	AG A	racac	GGAT	r	300
TACGACTA'	rg ci	ratgo	SACTA	A CTC	GGGG	CCAA	GGG	ACCA	CGG :	rcaco	CGTCT	rc c	ГСА			354
(2) INFO	RMAT	ON I	FOR S	SEQ 1	D NO):7:										
(i)	(B)	LEN TYI STR	IGTH: PE: & RANDE	ARACT 113 amino EDNES Y:]	ami aci SS: s	ino a id singl	acids	3								
(ii)	MOLE	ECULE	E TYP	PE: p	pepti	de										
(xi)	SEQU	JENCE	E DES	SCRIE	PTION	l: SI	EQ II	ONO:	:7: [′]							
Asp 1	Val	Leu	Met	Thr 5	Gln	Thr	Pro	Leu	Ser 10	Leu	Pro	Val	Asn	Ile 15	Gly	
Asp	Gln	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Thr	Lys	Ser	Leu	Leu	Asn	Ser	

Asp Gly Phe Thr Tyr Leu Gly Trp Cys Leu Gln Lys Pro Gly Gln Ser 35 40 45

Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn Arg Phe Ser Gly Val Pro 50 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Ser 85 90 95	
Asn Tyr Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys 100 105 110	
Arg	
(2) INFORMATION FOR SEQ ID NO:8:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA to mRNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
GATGTTTTGA TGACCCAAAC TCCACTCTCT CTGCCTGTCA ATATTGGAGA TCAAGCCTCT	60
ATCTCTTGCA AGTCTACTAA GAGCCTTCTG AATAGTGATG GATTCACTTA TTTGGGCTGG	120
TGCCTGCAGA AGCCAGGCCA GTCTCCACAG CTCCTAATAT ATTTGGTTTC TAATCGATTT	180
TCTGGAGTTC CAGACAGGTT CAGTGGTAGT GGGTCAGGGA CAGATTTCAC CCTCAAGATC	240
AGCAGAGTGG AGGCTGAGGA TTTGGGAGTT TATTATTGCT TCCAGAGTAA CTATCTTCCT	300
CTTACGTTCG GATCGGGGAC CAAGCTGGAA ATAAAACGG	339
(2) INFORMATION FOR SEQ ID NO:9:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: peptide	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser 1 5 10 15	
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Trp 20 25 30	
Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile Gly 35 40 45	
Arg Ile Tyr Pro Val Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys 50 55 60	
Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met 65 70 75 80	
Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala	

Thr	Asp	Gly	Tyr	Trp	Tyr	Phe	Asp	Val	\mathtt{Trp}	Gly	Gln	Gly	Thr	Thr	Val
			100					105				_	110		

Thr Val Ser Ser 115

(2)	INFORMATION	FOR	SEO	TD	NO - 10	

/ i) 01	POSTENCE	CHARACTERISTICS
1 1	1 51	*.()() *.	CHARACTERISTICS

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGAAGCTGC	AGGAGTCTGG	ACCTGAGCTG	GTGAAGCCTG	GGGCCTCAGT	GAAGATTTCC	60
TGCAAGGCTT	CTGGCTATGC	ATTCAGTAGC	TCCTGGATGA	ACTGGGTGAA	ACAGAGGCCT	120
GGGAAGGGTC	TTGAGTGGAT	TGGACGGATT	TATCCTGTAA	ATGGAGATAC	TAACTACAAT	180
GGGAAGTTCA	AGGGCAAGGC	CACACTGACT	GCAGACAAAT	CCTCCAGCAC	AGCCTACATG	240
CAACTCAGCA	GCCTGACATC	TGAGGACTCT	GCGGTCTACT	TCTGTGCAAC	CGATGGTTAC	300
TGGTACTTCG	ATGTCTGGGG	CCAAGGGACC	ACGGTCACCG	TCTCCTCA		348

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Ser

Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly Tyr

Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met

Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys

Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe Leu

Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala 85 90 95

V	ai Tyr	Tyr	19r 100	Asp	GIÀ	ser	Ser	105	Asp	Tyr	Trp	GIY	110	Gly	Thr	
Tì	nr Val	Thr 115	Val	Ser	Ser											
(2) IN	FORMAT	ION I	FOR S	SEQ :	ID N	0:12	:									
(:	(B (C	UENC:) LEI) TY:) STI	NGTH PE: 1 RANDI	: 354 nucle EDNE	4 bas eic a SS: o	se pa acid doub	airs									
(i:	L) MOL	ECUL	E TYI	PE: (cDNA	to 1	πRNA									
(x :	L) SEQ	UENC	E DES	SCRI	PTIO	N: S	EQ II	ONO:	:12:							
GTGCAG	CTGC A	.GGAG	rctg	G AC	CTGG	CCTC	GTG	AAAC	CTT (CTCAC	TCT	CT G	rctc:	CAC	C	60
TGCTCTC	TCA C	TGGC'	TACTO	CA'	TCAC	CAGT	GGT	TATTA	ACT (GGAA	CTGG	AT C	CGGC	AGTT:	Г	120
CCAGGA	AACA A	ACTG	GAATO	G GA	TGGG	CTAC	ATA	AGCT	ACG A	ATGGT	[AGC	AA TA	AACT	ACAA	2	180
CCATCT	CTCA A	AAAT	CGAA:	r ct	CCAT	CACT	CGT	GACA	CAT (CTAAC	BAAC	CA G	rttt:	rccto	3	240
AAGTTG	AATT C	TGTG	ACTA	C TG	AGGA	CACA	GCC	ACATA	ATT A	ACTGT	rgcc	GT T	TATTA	ACTA	2	300
GATGGT	GCT C	TTTT	GACTA	A CTO	GGGG	CCAA	GGGZ	ACCA	CGG :	CAC	CGTC	rc c	ГСА			354
(2) IN	ORMAT	ION 1	FOR S	SEQ :	ID NO	0:13	:									
(:	(B (C	UENCI) LEI) TYI) STI) TOI	NGTH PE: a RANDI	: 112 amino EDNES	2 am: 5 ac: 88: 8	ino a id sing!	acids	5								
(i:) MOL	ECULI	E TYI	PE: 1	pept:	ide										
(xi	.) SEQ	UENCI	E DES	SCRII	PTIO	N: SI	EQ II	ONO:	:13:							
As 1	sp Ile	Val	Leu	Thr 5	Gln	Ser	Pro	Ala	Ser 10	Leu	Ala	Val	Ser	Leu 15	Arg	
G]	n Arg	Ala	Thr 20	Ile	Ser	Cys	Arg	Ala 25	Ser	Glu	Gly	Val	Asp 30	Ser	Tyr	
G	y Ile	Ser 35	Phe	Met	His	Trp	Tyr 40	Gln	Gln	Lys	Pro	Gly 45	Gln	Pro	Pro	
L	s Leu 50	Leu	Ile	Tyr	Arg	Ala 55	Ser	Tyr	Leu	Lys	Ser 60	Gly	Val	Pro	Ala	
` A:	g Phe	Ser	Gly	Ser	Gly 70	Ser	Arg	Thr	Asp	Phe 75	Thr	Leu	Thr	Ile	Asp 80	
Pı	o Val	Glu	Ala	Asp 85	Asp	Ala	Ala	Thr	Tyr 90	Tyr	Cys	Gln	Gln	Asn 95	Asn	
G]	u Asp	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	

(2)

100	105	•	110

(2) INFOR	MAT:	ION I	FOR S	SEQ I	D NO	0:14	:								
(i)	(A) (B) (C)	LEI TYI STI	E CHANGTH: PE: 1 RANDE	: 336 nucle EDNES	bas bic a ss: c	se pa acid doub!	airs								
(ii)	MOLI	ECULI	TYP	PE: c	DNA	to r	nRNA							•	
(xi)	SEQU	JENCI	E DES	SCRIE	OITS	J: SI	EQ II	O NO:	:14:						
GACATTGTG										CTCTA	AAGGG	CA GA	AGGGG	CCACC	2
ATATCCTGC	'A G	AGCCZ	AGTGA	A AGO	TGT	GAT	AGT	ratgo	GCA 1	TAG	TTTT	AT GO	CACTO	GTAC	2
CAGCAGAAA	C C	AGGA	CAGCO	C ACC	CCAA	ACTC	CTC	ATCT!	ATC (STGC	ATCCI	ra co	CTAAA	ATCI	ľ
GGGGTCCCT	G CC	CAGGI	TCAC	TGC	TAG	rggg	TCT	AGGA	CAG A	ACTTO	CACCO	T C	ACCAI	TGAT	ŗ
CCTGTGGAG	G CI	rgato	ATGO	TG0	CAAC	CTAT	TACT	rgtc <i>i</i>	AGC A	LAAA	TAATO	A GO	SATCO	CGTGC	3
ACGTTCGGT	G GI	AGGC	ACCA	A GCT	rgga <i>i</i>	ATC	AAA	CGG							
(2) INFOR	TAM	ON I	FOR S	SEQ]	D NO):15:	:								
(i)	(A) (B) (C)	LEN TYP STF	E CHA IGTH: PE: a RANDE	: 117 amino EDNES	7 ami 5 aci 5S: s	no a d singl	acids	3							
(ii)	MOLE	ECULE	E TYP	E: p	epti	de									
(xi)	SEQU	JENCE	E DES	CRIE	OIT	I: SE	EQ II	NO:	15:						
Val 1	Gln	Leu	Gln	Glu 5	Ser	Gly	Ala	Glu	Pro 10	Ala	Lys	Pro	Gly	Ala 15	Ser
Val	Lys	Met	Ser 20	Cys	Lys	Ala	Ser	Gly 25	Tyr	Thr	Phe	Thr	Thr 30	Tyr	Trp
Met	His	Trp 35	Val	Lys	Gln	Arg	Pro 40	Gly	Gln	Gly	Leu	Glu 45	Trp	Ile	Gly
Tyr	Ile 50	Asn	Pro	Ser	Ser	Gly 55	Tyr	Thr	Glu	Tyr	Asn 60	Gln	Lys	Phe	Lys
Asp 65	Lys	Ala	Thr	Leu	Thr 70	Ala	Asp	Lys	Ser	Ser 75	Ser	Thr	Ala	Tyr	Met 80
Gln	Leu	Ile	Ser	Leu 85	Thr	Ser	Glu	Asp	Ser 90	Ala	Val	Tyr	Tyr	Cys 95	Ala
Arg	Arg	Gly	Asn 100	Tyr	Tyr	Tyr	Phe	Asp 105	Tyr	Trp	Gly	Gln	Gly 110	Thr	Thr

Val Thr Val Ser Ser

(2) INFORMATION FOR SEQ ID NO:16:											
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 											
(ii) MOLECULE TYPE: cDNA to mRNA											
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:											
GTGCAGCTGC AGGAGTCTGG GGCTGAACCG GCAAAACCTG GGGCCTCAGT GAAGATGTCC											
TGCAAGGCTT CTGGCTACAC CTTTACTACC TACTGGATGC ACTGGGTAAA ACAGAGGCCT											
GGACAGGGTC TGGAATGGAT TGGATACATT AATCCTAGCA GTGGTTATAC TGAGTACAAT											
CAGAAGTTCA AGGACAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG											
CAACTAATCA GCCTGACATC TGAGGACTCT GCAGTCTATT ACTGTGCAAG AAGGGGTAAT											
TACTACTACT TTGACTACTG GGGCCAAGGG ACCACGGTCA CCGTCTCCTC A											
(2) INFORMATION FOR SEQ ID NO:17:											
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 											
(ii) MOLECULE TYPE: peptide											
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:											
Asp Val Leu Met Thr Gln Thr Pro Lys Phe Leu Pro Val Ser Ala Gly 1 5 10 15											
Asp Arg Val Thr Met Thr Cys Lys Ala Ser Gln Ser Val Gly Asn Asn 20 25 30											
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile 35 40 45											
Tyr Tyr Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly 50 55 60											
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Val 65 70 75 80											
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Tyr Ser Ser Pro Tyr 85 90 95											
Thr Phe Gly Ser Gly Thr Lys Leu Glu 100 105											

(2) INFORMATION FOR SEQ ID NO:18:

	(D)	TOI	POLO	3Y: :	line	ar									
(ii)	MOLI	ECULI	E TY	PE: (cDNA	to r	mRNA								
(20)	CEOI	יייייייי	ישרו ב	COT	חתדים	vī. (1)	EO T	- NO	1.0						
(xi)															
GATGTTTT	GA TO	GACC	CAAA	C TC	CAAA	ATTC	CTG	CCTG'	TAT (CAGC	AGGA	GA C	AGGG:	rtac(C
ATGACCTG	CA A	3GCC2	AGTC	A GA	GTGT(GGT	AAT	AATG:	rgg (CCTG	GTAC(CA A	CAGA	AGCC	A
GGACAGTCTC CTAAACTGCT GATATACTAT ACATCCAATC GCTACACTGG AGTCCCTGAT															
CGCTTCAC	rg go	CAGTO	GGAT	TG	GGAC	AGAT	TTC	ACTT	CA (CCAT	CAGC	AG T	GTGC	AGGT	Γ
GAAGACCT	GG CI	AGTTT	ratt:	CTC	GTCA	GCAG	CAT	CATA	GCT (CTCC	TAT	AC G	rtcg	GATC	3
GGGACCAA	GC TO	GGAG													
(2) INFO	RMAT	ION I	FOR S	SEQ :	ID NO	0:19	:								
(i)	(A) (B) (C)	LEN TYP STF	NGTH: PE: 8 RANDE	: 12: amino EDNES	TERIS L am: b ac: SS: s Lines	ino a id sing:	acids	5							
(ii)	MOLE	CULE	TYI	PE: 1	pept:	ide									
											•				
(xi)	SEQU	JENCE	E DES	CRI	PTIO	N: SI	EQ II	ON C	:19:						
Gln 1	Val	Gln	Leu	Gln 5	Gln	Ser	Gly	Pro	Glu 10	Leu	Val	Lys	Pro	Gly 15	Ala
Ser	Val	Lys	Ile 20	Ser	Cys	Lys	Ala	Ser 25	Gly	Tyr	Ala	Phe	Ser 30	Ser	Ser
Trp	Met	Asn 35	Trp	Val	Lys	Gln	Arg 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Ile
Gly	Arg 50	Ile	Tyr	Pro	Gly	Asp 55	Gly	Asp	Thr	Asn	Asp 60	Asn	Gly	Lys	Phe
Lys 65	Gly	Lys	Ala	Thr	Leu 70	Thr	Ala	Asp	Lys	Ser 75	Ser	Ser	Thr	Ala	Tyr 80
Met	Gln	Leu	Ser	Ser 85	Leu	Thr	Ser	Glu	Asp 90	Ser	Ala	Val	Tyr	Phe 95	Cys
Ala	Arg	Ser	Tyr 100	Tyr	Tyr	Asp	Gly	Ser 105	Pro	Trp	Phe	Thr	Tyr 110	Trp	Gly
Gln	Gly	Thr 115	Leu	Val	Thr	Val	Ser 120	Ala		ν.	-				

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(xi) S	SEQUENCE	E DESCRI	PTION: S	EQ I	NO:	20:							
CAGGTTCAGC	C TGCAG	CAGTC TG	GACCTGAG	CTG	GTGAA	.GC (CTGGG	GCCI	C AC	STGA	AGAT:	Г	60
TCCTGCAAGG	CTTCT	GCTA TG	CATTCAGI	' AGC'	rcctg	GA T	rga a 0	TGGG	T G	AAGC	AGAG	3	120
CCTGGAAAGG	GTCTT	GAGTG GA	TTCGAATT	TAT	CCTGG	AG A	ATGG	GATA	C T	AACG	ACAA	2	180
GGGAAGTTCA	A AGGGA	GCAA GG	CCACACTG	ACC	GCAGA	CA A	ATC	TCCA	G C	ACAG	CCTAC	2	240
ATGCAACTCA	GCAGT	CTGAC AT	CTGAGGAC	TCT	GCGGT	'CT I	ACTTO	TGTG	C A	AGAT	CGTAT	Г	300
TACTACGATG	GTAGC	CCCTG GT	TTACTTAC	TGG	GGCCA	AG (GACI	CTGG	T C	ACTG	CTC	r	360
GCA													363
(2) INFORM	MATION E	FOR SEQ	ID NO:21	:									
(i) SEQUENCE CHARACTERISTICS:													
(xi) S	SEQUENCE	E DESCRI	PTION: S	EQ II	NO:	21:							
Asp I 1	le Gln	Met Thr 5	Gln Thr	Thr	Ser	Ser 10	Leu	Ser	Ala	Ser	Leu 15	Gly	
Asp A	arg Val	Thr Ile 20	Ser Cys	Arg	Ala 25	Ser	Gln	Asp	Ile	Ser 30	Asn	Tyr	
Leu A	sn Trp 35	Tyr Gln	Gln Lys	Pro 40	Asp	Gly	Thr	Val	Lys 45	Leu	Leu	Ile	
	Tyr Thr	Ser Arg	Leu His	Ser	Gly	Val	Pro	Ser 60	Arg	Phe	Ser	Gly	
Ser G 65	Sly Ser	Gly Thr	Asp Tyr	Ser	Leu	Thr	Ile 75	Ser	Asn	Leu	Glu	Pro 80	
Glu A	asp Ile	Ala Thr 85	Tyr Phe	Cys	Gln	Gln 90	Tyr	Ser	Glu	Phe	Pro 95	Trp	
Thr P	he Gly	Gly Gly 100	Thr Lys	Leu	Glu 105	Ile	Lys	Arg					

(A) LENGTH: 363 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs (B) TYPE: nucleic acid

(XI)	SEQU	JENCE	s DES	SCRII	PTION	v: Si	EQ II	ON C	:22:						
GATATCCAG	A TO	BACAC	CAGA	TAC	CATC	CTCC	CTG	CTG	CCT (CTCTC	GGA	GA C	AGAG	CAC	2
ATCAGTTGC	A GG	GCA	AGTC	A GGA	TAT	ragc	AAT	TATT?	raa A	ACTGO	TAT	CA G	CAGA	AACC	A
GATGGAACT	G TI	'AAAC	CTCC	r GAT	CTAC	CTAC	ACA	CAA	GAT :	TACAC	CTCA	GG A	GTCC	CATC	A
AGGTTCAGT	G GC	CAGTO	GGT	TGC	GAC	AGAT	TAT	CTC:	CA (CCATO	CAGC	AA C	CTGG	AACCI	ŗ
GAAGATATTG CCACTTACTT TTGTCAGCAA TATAGTGAAT TTCCGTGGAC GTTCGGTGGA															
GGCACCAAGC TGGAAATCAA ACGG															
(2) INFOR	(2) INFORMATION FOR SEQ ID NO:23:														
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 119 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear															
(ii)	MOLE	CULE	E TYI	E: p	epti	ide									
(xi)	SEQU	JENCE	E DES	SCRIE	OITS	J: SE	EQ II	NO:	23:						
Gln 1	Val	His	Leu	Gln 5	Gln	Ser	Gly	Ala	Glu 10	Leu	Val	Arg	Pro	Gly 15	Thr
Ser	Val	Lys	Met 20	Ser	Cys	Lys	Ala	Ala 25	Gly	Tyr	Thr	Phe	Thr 30	Asn	Tyr
Trp	Ile	Gly 35	Trp	Val	Lys	Gln	Arg 40	Pro	Gly	His	Gly	Leu 45	Glu	Trp	Ile
Gly	Tyr 50	Leu	Tyr	Pro	Gly	Gly 55	Leu	Tyr	Thr	Asn	Tyr 60	Asn	Glu	Lys	Phe
Lys 65	Gly	Lys	Ala	Thr	Leu 70	Thr	Ala	Asp	Thr	Ser 75	Ser	Ser	Thr	Ala	Tyr 80
Met	Gln	Leu	Ser	Ser 85	Leu	Thr	Ser	Glu	Asp 90	Ser	Ala	Ile	Tyr	Tyr 95	Cys
Ala	Arg	Tyr	Arg 100	Asp	Tyr	Asp	Tyr	Ala 105	Met	Asp	Tyr	Trp	Gly 110	Gln	Gly
Thr	Ser	Val 115	Thr	Val	Ser	Ser									
(2) INFOR	MATI	ON F	FOR S	SEQ]	D NO):24:	:								

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOL	OGY:	linear
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(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGGTCCACC	TGCAGCAGTC	TGGAGCTGAG	CTGGTAAGGC	CTGGGACTTC	AGTGAAGATG	60
TCCTGCAAGG	CTGCTGGATA	CACCTTCACT	AACTACTGGA	TAGGTTGGGT	AAAGCAGAGG	120
CCTGGACATG	GCCTTGAGTG	GATTGGATAT	CTTTACCCTG	GAGGTCTTTA	TACTAACTAC	180
AATGAGAAGT	TCAAGGGCAA	GGCCACACTG	ACTGCAGACA	CATCCTCCAG	CACAGCCTAC	240

300

357

ATGCAGCTCA GCAGCCTGAC ATCTGAGGAC TCTGCCATCT ATTACTGTGC AAGATACAGG

GATTACGACT ATGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCACCGT CTCCTCA

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp Val Val Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Asn Ile Gly

Asp Gln Ala Ser Ile Ser Cys Lys Ser Thr Lys Ser Leu Leu Asn Ser

Asp Gly Phe Thr Tyr Leu Gly Trp Cys Leu Gln Lys Pro Gly Gln Ser

Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn Arg Phe Ser Gly Val Pro

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Ser 90

Asn Tyr Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys

Arg

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:									
GATGTTGTTC TGACCCAAAC TCCACTCTCT CTGCCTGTCA ATATTGC	GAGA TCAAGCCTCT 60								
ATCTCTTGCA AGTCTACTAA GAGCCTTCTG AATAGTGATG GATTCAG	CTTA TTTGGGCTGG 120								
TGCCTGCAGA AGCCAGGCCA GTCTCCACAG CTCCTAATAT ATTTGG	TTTC TAATCGATTT 180								
TCTGGAGTTC CAGACAGGTT CAGTGGTAGT GGGTCAGGGA CAGATT	TCAC CCTCAAGATC 240								
AGCAGAGTGG AGGCTGAGGA TTTGGGAGTT TATTATTGCT TCCAGAG	GTAA CTATCTTCCT 300								
CTTACGTTCG GATCGGGGAC CAAGCTGGAA ATAAAACGG	339								
(2) INFORMATION FOR SEQ ID NO:27:									
(i) SEQUENCE CHARACTERISTICS:									
(A) LENGTH: 117 amino acids (B) TYPE: amino acid									
(C) STRANDEDNESS: single									
(o, olicaloudingto									

(ii) MOLECULE TYPE: peptide

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile 35 40

Gly Arg Ile Tyr Pro Val Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys 85 90 95

Ala Thr Asp Gly Tyr Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
100 105 110

Val Thr Val Ser Ser 115

- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA

(xi)	SEQUENCE DES	CRIPTION: S	EQ ID NO:28	:		
CAGGTTCAG	GC TGCAGCAGTC	TGGACCTGAG	CTGGTGAAGC	CTGGGGCCTC	AGTGAAGATT	60
rcctgcaa(GG CTTCTGGCTA	TGCATTCAGT	AGCTCCTGGA	TGAACTGGGT	GAAACAGAGG	120
CCTGGGAAG	GG GTCTTGAGTG	GATTGGACGG	ATTTATCCTG	TAAATGGAGA	TACTAACTAC	180
AATGGGAA	GT TCAAGGGCAA	GGCCACACTG	ACTGCAGACA	AATCCTCCAG	CACAGCCTAC	240
ATGCAACT	CA GCAGCCTGAC	ATCTGAGGAC	TCTGCGGTCT	ACTTCTGTGC	AACCGATGGT	300
TACTGGTA	CT TCGATGTCTG	GGGCGCAGGG	ACCACGGTCA	CCGTCTCCTC	A	351
(2) INFOR	RMATION FOR S	EO ID NO:29	:			

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly

Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ile Tyr 25

Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile

Tyr Gly Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ala

Glu Asp Leu Ser Asp Tyr Tyr Cys Val Gln Ser Tyr Ser Tyr Pro Trp

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AACATTGTAA	TGACCCAATC	TCCCAAATCC	ATGTCCATGT	CAGTAGGAGA	GAGGGTCACC	60
TTGAGCTGCA	AGGCCAGTGA	GAATGTGGAT	ATTTATGTAT	CCTGGTATCA	ACAGAAACCA	120
GAGCAGTCTC	CTAAACTGCT	GATATACGGG	ACATCCAACC	GGTACACTGG	GGTCCCCGAT	180
CGCTTCACAG	GCAGTGGATC	TGCAACAGAT	TTCACTCTGA	CCATCAGCAA	TGTGCAGGCT	240
GAAGACCTTT	CAGATTATTA	CTGTGTACAG	AGTTACAGCT	ATCCGTGGAC	ATTCGGTGGA	300
GGCACCAAGC	TGGAAATCAA	ACGG				324

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln